

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Linemeyer, David L.
Menke, John G.
Hess, John F.
Borkowski, Joseph A.
Bierillo, Kathleen K.

(ii) TITLE OF INVENTION: DNA ENCODING BRADYKININ B1 RECEPTOR

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: John W. Wallen III
(B) STREET: P.O. Box 2000
(C) CITY: Rahway
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07065

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Wallen III, John W.
(B) REGISTRATION NUMBER: 35,403
(C) REFERENCE/DOCKET NUMBER: 19202

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (908) 594-3905
(B) TELEFAX: (908) 594-4720

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGAGAAAAC TCCTCCAAAA GCAGCTCTCA CTATCAGAAA ACCCAACTAC AGTTGTGAAC	60
GCCTTCATTT TCTGCCTGAG GTCTCAGTCC GTCGGCCAG ACTGAAGTGC AGTGGCACAA	120
TCATAGCTCG CTGCAGCCTC GACCTTCCAG GCTTAAACGA TTCTCCCACC TCAGCCTCTC	180
GAGTTGCTGG GACCACAGGT CACTGTGCAT GGCATCATCC TGGCCCCCTC TAGAGCTCCA	240
ATCCTCCAAC CAGAGCCAGC TCTTCCCTCA AAATGCTACG GCCTGTGACA ATGCTCCAGA	300
AGCCTGGGAC CTGCTGCACA GAGTGCTGCC GACATTTATC ATCTCCATCT GTTTCTTCGG	360
CCTCCTAGGG AACCTTTTTG TCCTGTTGGT CTTCCTCCTG CCCCGGCGGC AACTGAACGT	420
GGCAGAAATC TACCTGGCCA ACCTGGCAGC CTCTGATCTG GTGTTTGTCT TGGGCTTGCC	480
CTTCTGGGCA GAGAATATCT GGAACCAGTT TAACTGGCCT TTCGGAGCCC TCCTCTGCCG	540
TGTCATCAAC GGGGTCATCA AGGCCAATTT GTTCATCAGC ATCTTCCTGG TGGTGGCCAT	600
CAGCCAGGAC CGCTACCGCG TGCTGGTGCA CCCTATGGCC AGCGGAAGGC AGCAGCGGCG	660
GAGGCAGGCC CGGGTCACCT GCGTGCTCAT CTGGGTGTG GGGGGCCTCT TGAGCATCCC	720
CACATTCCTG CTGCGATCCA TCCAAGCCGT CCCAGATCTG AACATCACCG CCTGCATCCT	780
GCTCCTCCCC CATGAGGCCT GGCACCTTGC AAGGATTGTG GAGTTAAATA TTCTGGGTTT	840
CCTCCTACCA CTGGCTGCGA TCGTCTTCTT CAACTACCAC ATCCTGGCCT CCCTGCGAAC	900
GCGGGAGGAG GTCAGCAGGA CAAGGTGCGG GGGCCGCAAG GATAGCAAGA CCACAGCGCT	960
GATCCTCAGC CTCGTGGTTG CTTTCCTGGT CTGCTGGGCC CCTTACCACT TCTTTGCCCT	1020
CCTGGAATTC TTATTCCAGG TGCAAGCAGT CCGAGGCTGC TTTTGGGAGG ACTTCATTGA	1080
CCTGGGCCTG CAATTGGCCA ACTTCTTTGC CTTCACTAAC AGCTCCCTGA ATCCAGTAAT	1140
TTATGTCTTT GTGGGCCGGC TCTTCAGGAC CAAGGTCTGG GAACTTTATA AACAATGCAC	1200
CCCTAAAAGT CTTGCTCCAA TATCTTCATC CCATAGGAAA GAAATCTTCC AACTTTTCTG	1260
GCGGAATTAA AACAGCATTG AACCAAGAAA AAAAAAAAAA AAAAAAA	1307

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

Met 1	Ala	Ser	Ser	Trp 5	Pro	Pro	Leu	Glu	Leu 10	Gln	Ser	Ser	Asn	Gln	Ser
Gln	Leu	Phe	Pro 20	Gln	Asn	Ala	Thr	Ala 25	Cys	Asp	Asn	Ala	Pro 30	Glu	Ala
Trp	Asp	Leu 35	Leu	His	Arg	Val	Leu 40	Pro	Thr	Phe	Ile	Ile 45	Ser	Ile	Cys
Phe	Phe 50	Gly	Leu	Leu	Gly	Asn 55	Leu	Phe	Val	Leu	Leu 60	Val	Phe	Leu	Leu
Pro 65	Arg	Arg	Gln	Leu	Asn 70	Val	Ala	Glu	Ile	Tyr 75	Leu	Ala	Asn	Leu	Ala 80
Ala	Ser	Asp	Leu	Val 85	Phe	Val	Leu	Gly	Leu 90	Pro	Phe	Trp	Ala	Glu 95	Asn
Ile	Trp	Asn	Gln 100	Phe	Asn	Trp	Pro	Phe 105	Gly	Ala	Leu	Leu	Cys 110	Arg	Val
Ile	Asn	Gly 115	Val	Ile	Lys	Ala	Asn 120	Leu	Phe	Ile	Ser	Ile 125	Phe	Leu	Val
Val 130	Ala	Ile	Ser	Gln	Asp	Arg 135	Tyr	Arg	Val	Leu	Val 140	His	Pro	Met	Ala
Ser 145	Gly	Arg	Gln	Gln	Arg	Arg 150	Arg	Gln	Ala	Arg	Val 155	Thr	Cys	Val	Leu 160
Ile	Trp	Val	Val 165	Gly	Gly	Leu	Leu	Ser	Ile 170	Pro	Thr	Phe	Leu	Leu 175	Arg
Ser	Ile	Gln	Ala 180	Val	Pro	Asp	Leu	Asn 185	Ile	Thr	Ala	Cys	Ile 190	Leu	Leu
Leu	Pro	His 195	Glu	Ala	Trp	His	Phe 200	Ala	Arg	Ile	Val	Glu 205	Leu	Asn	Ile
Leu	Gly 210	Phe	Leu	Leu	Pro	Leu 215	Ala	Ala	Ile	Val	Phe 220	Phe	Asn	Tyr	His
Ile 225	Leu	Ala	Ser	Leu	Arg 230	Thr	Arg	Glu	Glu	Val 235	Ser	Arg	Thr	Arg	Cys 240
Gly	Gly	Arg	Lys 245	Asp	Ser	Lys	Thr	Thr	Ala 250	Leu	Ile	Leu	Thr	Leu 255	Val
Val	Ala	Phe	Leu 260	Val	Cys	Trp	Ala	Pro 265	Tyr	His	Phe	Phe	Ala 270	Phe	Leu
Glu	Phe	Leu	Phe	Gln	Val	Gln	Ala	Val	Arg	Gly	Cys	Phe	Trp	Glu	Asp

275	280	285	
Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn			
290	295	300	
Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg			
305	310	315	320
Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala			
	325	330	335
Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg			
	340	345	350

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